GenCore version 4.5

OM protein - protein search, using sw model

Run on: April 24, 2002, 10:37:58 ; Search time 71.56 Seconds
(without alignments)
82.491 Million cell updates/sec

Title: US-09-525-998A-2_COPY_41_201
Perfect score: 941
Sequence: 1 DSVCPQGKYIHPQNNSICCT..........CSNCKKSLECTKLCLPQIEN 161

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	941	100.0	455	1	TNR1_HUMAN	P19438 homo sapien
2	716.5	76.1	461	1	TNR1_PIG	P50555 sus scrofa
3	680	72.3	454	1	TNR1_MOUSE	P25118 mus musculu
4	674.5	71.7	471	1	TNR1_BOVIN	O19131 bos taurus
5	669	71.1	461	1	TNR1_RAT	P22934 rattus norv
6	200.5	21.3	417	1	WSL1_HUMAN	Q93038 h wsl-1 pro
7	187.5	19.9	435	1	TNRC_HUMAN	P36941 homo sapien
8	182.5	19.4	427	1	NGFR_HUMAN	P08138 homo sapien
9	181	19.2	474	1	TNR2_MOUSE	P25119 mus musculu
10	179.5	19.1	326	1	VT2_MYXVL	P29825 myxoma viru
11	178	18.9	325	1	VT2_SFVKA	P25943 shope fibro
12	176.5	18.8	332	1	FASA_PIG	O77736 sus scrofa
13	176.5	18.8	425	1	NGFR_RAT	P07174 rattus norv
14	167.5	17.8	289	1	CD40_MOUSE	P27512 mus musculu
15	167.5	17.8	415	1	TNRC_MOUSE	P50284 mus musculu
16	167	17.7	269	1	CD40_BOVIN	Q28203 bos taurus
17	166.5	17.7	323	1	FASA_BOVIN	P51867 bos taurus
18	164	17.4	349	1	VC22_VARV	P34015 variola vir
19	162.5	17.3	327	1	FASA_MOUSE	P25446 mus musculu
20	161	17.1	461	1	TNR2_HUMAN	P20333 homo sapien
21	147	15.6	324	1	FASA_RAT	Q63199 rattus norv
22	145	15.4	416	1	NGFR_CHICK	P18519 gallus gall
23	142	15.1	283	1	TR14_HUMAN	Q92956 homo sapien
24	141	15.0	1680	1	FUP2_DROME	P30432 drosophila
25	139.5	14.8	250	1	CD27_MOUSE	P41272 mus musculu
26	139.5	14.8	277	1	CD40_HUMAN	P25942 homo sapien
27	138.5	14.7	260	1	CD27_HUMAN	P26842 homo sapien
28	134	14.2	1696	1	PCK5_BRACL	O9nj15 branchiosto
29	134	14.2	1877	1	PCK5_MOUSE	Q04592 mus musculu
30	133	14.1	687	1	VS41_GIALA	P92127 giardia lam
31	132	14.0	913	1	PCK5_HUMAN	Q92824 homo sapien
32	131.5	14.0	272	1	OX40_MOUSE	P47741 mus musculu
33	130.5	13.9	335	1	FASA_HUMAN	P25445 homo sapien
34	129	13.7	595	1	CD30_HUMAN	P28908 homo sapien
35	124	13.2	3672	1	LML2_CAEEL	Q21313 caenorhabdi
36	122.5	13.0	271	1	OX40_RAT	P15725 rattus norv
37	119	12.6	279	1	SLI3_MOUSE	O70433 mus musculu
38	116.5	12.4	277	1	OX40_HUMAN	P43489 homo sapien
39	116.5	12.4	892	1	LDL2_XENLA	Q99088 xenopus lae
40	116	12.3	279	1	SLI3_RAT	O35115 rattus norv
41	115.5	12.3	1712	1	TGFB_RAT	Q00918 rattus norv
42	115	12.2	279	1	SLI3_HUMAN	Q14192 homo sapien
43	115	12.2	2318	1	NTC3_MOUSE	Q61982 mus musculu
44	114	12.1	1790	1	LMB1_DROME	P11046 drosophila
45	113.5	12.1	220	1	ANTA_HYDMA	P58977 hydra magni

ALIGNMENTS

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RESULT 1
TNR1_HUMAN
ID   TNR1_HUMAN     STANDARD;      PRT;   455 AA.
AC   P19438;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   29-AUG-2001 (Rel. 40, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR
DE   BINDING PROTEIN 1) (TBP1) (P60) (TNF-R1) (TNF-RI) (P55) (CD120A).
GN   TNFRSF1A OR TNFR1 OR TNFAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=90235285; PubMed=2158863;
RA   Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,
RA   Gatanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;
RT   "Molecular cloning and expression of a receptor for human tumor
RT   necrosis factor.";
RL   Cell 61:361-370(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90235284; PubMed=2158862;
RA   Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,
RA   Tabuchi H., Lesslauer W.;
RT   "Molecular cloning and expression of the human 55 kd tumor necrosis
RT   factor receptor.";
RL   Cell 61:351-359(1990).
RN   [3]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 41-53, 110-124 AND 133-201.
RX   MEDLINE=91006021; PubMed=1698610;
RA   Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R.,
RA   Aderka D., Holtmann H., Wallach D.;
RT   "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
RT   for the type I TNF-R, cloned using amino acid sequence data of its
RT   soluble form, encodes both the cell surface and a soluble form of the
RT   receptor.";
RL   EMBO J. 9:3269-3278(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91090941; PubMed=1702294;
RA   Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA   Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT   "Molecular cloning and expression of human and rat tumor necrosis
RT   factor receptor chain (p60) and its soluble derivative, tumor
RT   necrosis factor-binding protein.";
RL   DNA Cell Biol. 9:705-715(1990).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=91017595; PubMed=2170974;
RA   Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;
RT   "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
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RT   Expression of recombinant soluble TNF-binding protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92250049; PubMed=1315717;
RA   Fuchs P., Strehl S., Dworzak M., Himmler A., Ambros P.F.;
RT   "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
RT   localization to chromosome 12p13.";
RL   Genomics 13:219-224(1992).
RN   [7]
RP   SEQUENCE OF 41-45.
RX   MEDLINE=90110215; PubMed=2154136;
RA   Engelmann H., Novick D., Wallach D.;
RT   "Two tumor necrosis factor-binding proteins purified from human
RT   urine. Evidence for immunological cross reactivity with cell surface
RT   tumor necrosis factor receptors.";
RL   J. Biol. Chem. 265:1531-1536(1990).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.
RX   MEDLINE=93258809; PubMed=8387891;
RA   Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,
RA   Broger C., Loetscher H., Lesslauer W.;
RT   "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
RT   beta complex: implications for TNF receptor activation.";
RL   Cell 73:431-445(1993).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX   MEDLINE=97094982; PubMed=8939750;
RA   Naismith J.H., Devine T.Q., Kohno H., Sprang S.R.;
RT   "Structures of the extracellular domain of the type I tumor necrosis
RT   factor receptor.";
RL   Structure 4:1251-1262(1996).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF
CC       NONCYTOCIDAL TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION
CC       OF THE ACID SPHINGOMYELINASE.
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAF2, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO
CC       THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
CC       NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.html"
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------
DR   EMBL; X55313; CAA39021.1; -.
DR   EMBL; M33294; AAA04210.1; -.
DR   EMBL; M58286; AAA36753.1; -.
DR   EMBL; M63121; AAA36754.1; -.
DR   EMBL; M75866; AAA61201.1; -.
DR   EMBL; M75864; AAA61201.1; JOINED.
DR   EMBL; M75865; AAA61201.1; JOINED.
DR   EMBL; M60275; AAA36756.1; -.
DR   EMBL; A21522; CAA01558.1; -.
DR   PIR; A34899; GQHUT1.
DR   PIR; A35010; A35010.
DR   PIR; S12057; S12057.
DR   PIR; A38208; A38208.
DR   PDB; 1TNR; 31-JUL-94.
DR   PDB; 1NCF; 07-DEC-95.
DR   PDB; 1EXT; 11-JAN-97.
DR   MIM; 191190; -.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis;
KW   3D-structure.
FT   SIGNAL       1     21
FT   CHAIN       22    455       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   CHAIN       41    291       TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT   DOMAIN      22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   212    234       POTENTIAL.
FT   DOMAIN     235    455       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      43    196       4 X TNFR-CYS.
FT   REPEAT      43     82       TNFR-CYS 1.
FT   REPEAT      83    125       TNFR-CYS 2.
FT   REPEAT     126    166       TNFR-CYS 3.
FT   REPEAT     167    196       TNFR-CYS 4.
FT   DOMAIN     338    348       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN     356    441       DEATH.
FT   DISULFID    44     58
FT   DISULFID    59     72
FT   DISULFID    62     81
FT   DISULFID    84     99
FT   DISULFID   102    117
FT   DISULFID   105    125
FT   DISULFID   127    143
FT   DISULFID   146    158
FT   DISULFID   149    166
FT   DISULFID   168    179
FT   DISULFID   182    191
FT   DISULFID   185    195
FT   CARBOHYD    54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   145    145       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   412    412       MISSING (IN REF. 4).
FT   CONFLICT   443    446       GPAA -> APP (IN REF. 4).
SQ   SEQUENCE   455 AA;  50494 MW;  4CEFBA96D03B8225 CRC64;


  Query Match             100.0%;  Score 941;  DB 1;  Length 455;
  Best Local Similarity   100.0%;  Pred. No. 5e-71;
  Matches  161;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 100

Qy      61 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 160

Qy     121 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIEN 161
           |||||||||||||||||||||||||||||||||||||||||||
Db     161 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIEN 201


RESULT   2
TNR1_PIG
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ID   TNR1_PIG        STANDARD;      PRT;   461 AA.
AC   P50555;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF R1) (TNF-R1)
DE   (P55).
GN   TNFRSF1A OR TNFR1.
OS   Sus scrota (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=96011645; PubMed=7590278;
RA   Suter B., Pauli U.H.;
RT   "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
RT   receptor.";
RL   Gene 163:263-266(1995).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAF2, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19994; AAC48499.1; -.
DR   HSSP; P19438; 1TNR.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   ProDom; PD000771; TNFR_c6; 1
DR   SMART; SM00005; DEATH; 1
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
FT   SIGNAL       1     21       POTENTIAL.
FT   CHAIN       22    461       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN      22    210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   211    233       POTENTIAL
FT   DOMAIN     234    461       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      43    195       4 X TNFR-CYS.
FT   REPEAT      43     82       TNFR-CYS 1.
FT   REPEAT      83    125       TNFR-CYS 2.
FT   REPEAT     126    166       TNFR-CYS 3.
FT   REPEAT     167    195       TNFR-CYS 4
FT   DOMAIN     340    350       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN     362    447       DEATH
FT   DISULFID    44     58       BY SIMILARITY.
FT   DISULFID    59     72       BY SIMILARITY.
FT   DISULFID    62     81       BY SIMILARITY.
FT   DISULFID    84     99       BY SIMILARITY.
FT   DISULFID   102    117       BY SIMILARITY.
FT   DISULFID   105    125       BY SIMILARITY.
FT   DISULFID   127    143       BY SIMILARITY.
FT   DISULFID   146    158       BY SIMILARITY.
FT   DISULFID   149    166       BY SIMILARITY.
FT   DISULFID   168    179       BY SIMILARITY.
FT   DISULFID   182    190       BY SIMILARITY.
FT   DISULFID   185    194       BY SIMILARITY.
FT   CARBOHYD    54     54       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    86     86       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   145    145       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   151    151       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   461 AA;  50696 MW;  CD72361EC600C9D43 CRC64;


  Query Match             76.1%;  Score 716.5;  DB 1;  Length 461;
  Best Local Similarity   77.4%;  Pred. No. 1.7e-52;
  Matches  320;  Conservative   12;  Mismatches   22;  Indels    1;  Gaps    1;

Qy        1 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 60
            :::::::: ::: :::::::::::::::::: ::: :: ::::::::::::::::::  ||
Db       41 ESLCPQGKYSHPQNNSICCTKCHKGTYLHNDCLGPGQDTDCRECESGSFTASENHLRQCL 100

Qy       61 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 120
            :::::: :: ::::: :::::::::::::::::: ::: :::: ::::: ::: : : :
Db      101 SCEQCRSEMGQVEISPCTVDRDTVCGCRKNQFRHYWSENLFQCFNCSLCLNGTVQLSCQE 160

Qy      121 KQNTVCTCHAGFFLRENECVSCSNCKKSLECEKEC 155
            :::::: ::::::::: ::::: ::: : :: ::
Db      161 KQNTVCTCHAGFFLRENECVSCSNCKKNLECTKEC 194


RESULT   3
TNR1_MOUSE
ID   TNR1_MOUSE     STANDARD;      PRT;   454 AA.
AC   P25118;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-R1)
DE   (P55).
GN   TNFRSF1A OR TNFR1 OR TNFR-1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91187885; PubMed=1849278;
RA   Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA   Wong G.H., Chen E.Y., Goeddel D.V.;
RT   "Cloning and expression of cDNAs for two distinct murine tumor
RT   necrosis factor receptors demonstrate one receptor is species
RT   specific.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91246378; PubMed=1645445;
RA   Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA   Copeland N.G., Jenkins N.A., Smith C.A.;
RT   "Molecular cloning and expression of the type 1 and type 2 murine
RT   receptors for tumor necrosis factor.";
RL   Mol. Cell. Biol. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91285014; PubMed=1647956;
RA   Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissonerghis A.M.,
RA   Gray P.W., Feldmann M., Foxwell B.M.J.;
RT   "Cloning, expression and cross-linking analysis of the murine p55
RT   tumor necrosis factor receptor.";
RL   Eur. J. Immunol. 21:1649-1656(1991).
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RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=92039815; PubMed=1657766;
RA   Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
RT   "Molecular cloning and expression of the mouse Tnf receptor type b ";
RL   Immunogenetics 34:338-340(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94245292; PubMed=8188324;
RA   Bebo B.F., Linthicum D.S.;
RT   "Nucleotide sequence of the TNF type I receptor from a mouse
RT   endothelioma cell line.";
RL   Immunogenetics 39:450-451(1994).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93156721; PubMed=8381516;
RA   Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.;
RT   "Genomic organization and promoter function of the murine tumor
RT   necrosis factor receptor beta gene.";
RL   Mol. Immunol. 30:165-175(1993).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY)
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAF2, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M60468; AAA39751.1; -.
DR   EMBL; M59377; AAA40464.1; -.
DR   EMBL; X59238; CAA41922.1; -.
DR   EMBL; X57796; CAA40936.1; -.
DR   EMBL; L26349; AAA59361.1; -.
DR   EMBL; M76656; AAA40465.1; -.
DR   EMBL; M88067; AAA40465.1; JOINED.
DR   EMBL; M76655; AAA40465.1; JOINED.
DR   PIR; A38634; GQMST1.
DR   PIR; S16677; S16677.
DR   PIR; S19021; S19021.
DR   HSSP; P19438; 1EXT.
DR   MGD; MGI:1314884; Tnfrsf1a.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
FT   SIGNAL       1     21       POTENTIAL.
FT   CHAIN       22    454       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN      22    212       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   213    235       POTENTIAL.
FT   DOMAIN     236    454       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      43    196       4 X TNFR-CYS.
FT   REPEAT      43     82       TNFR-CYS 1.
FT   REPEAT      83    125       TNFR CYS 2.
FT   REPEAT     126    166       TNFR-CYS 3.
FT   REPEAT     167    196       TNFR-CYS 4.
FT   DOMAIN     339    349       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN     356    441       DEATH.
FT   DISULFID    44     58       BY SIMILARITY.
FT   DISULFID    59     72       BY SIMILARITY.
FT   DISULFID    62     81       BY SIMILARITY.
FT   DISULFID    84     99       BY SIMILARITY.
FT   DISULFID   102    117       BY SIMILARITY.
FT   DISULFID   105    125       BY SIMILARITY.
FT   DISULFID   127    143       BY SIMILARITY.
FT   DISULFID   146    158       BY SIMILARITY.
FT   DISULFID   149    166       BY SIMILARITY.
FT   DISULFID   168    179       BY SIMILARITY.
FT   DISULFID   182    191       BY SIMILARITY.
FT   DISULFID   185    195       BY SIMILARITY.
FT   CARBOHYD    54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   202    202       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   394    394       R -> G (IN REF. 6).
SQ   SEQUENCE   454 AA;  50129 MW;  0710C2E9C3C2B6D9 CRC64;
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  Query Match             72.3%;  Score 680;  DB 1;  Length 454;
  Best Local Similarity   71.3%;  Pred. No. 1.7e-49;
  Matches  112;  Conservative   19;  Mismatches   25;  Indels    0;  Gaps    0;

Qy       1 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 60
           ||:|||||||:| :|||||||||||||||| .||| ||.|| ||||| |:||||:|:|| ||
Db      41 DSLCPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCL 100

Qy      61 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 120
           ||  |||| |||| | |:|||||::||:: | ||  ||| :|| | |||| : |:|
Db     101 SCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160

Qy     121 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLP 157
           ||||| ||||||||:||| ||:||| || |||||
Db     161 TQNTVCNCHAGFFLRESECVPCSHCKKNEECMKLCLP 197
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RESULT   4
TNR1_BOVIN
ID   TNR1_BOVIN     STANDARD;      PRT;   471 AA.
AC   O19131;
DT   20 AUC 2001 (Rel. 40, Created)
DT   20-AUG-2001 (Rel. 40, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-RI)
DE   (P55).
GN   TNFRSF1A OR TNFR1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aorta;
RA   Lee E.-K., Talyor M.J., Kehrli M.E.;
RT   "Cloning of cDNA encoding bovine tumor necrosis factor-receptor I
RT   (TNF-RI).";
RL   Submitted (FEB 1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
```

```
CC        PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC    -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC        HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC        PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC        WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC        PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC        TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC        ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC        NF-KAPPA B SIGNALING (BY SIMILARITY).
CC    -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC    -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC    -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC    --------------------------------------------------------------------------
CC    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC    the European Bioinformatics Institute. There are no restrictions on its
CC    use by non-profit institutions as long as its content is in no way
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CC    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC    or send an email to license@isb-sib.ch).
CC    --------------------------------------------------------------------------
DR    EMBL; U90937; AAB65143.1; -.
DR    HSSP; P19438; 1TNR.
DR    InterPro; IPR000488; Death.
DR    InterPro; IPR001368; TNFR_c6.
DR    Pfam; PF00531; death; 1.
DR    Pfam; PF00020; TNFR_c6; 3.
DR    ProDom; PD000771; TNFR_c6; 1.
DR    SMART; SM00005; DEATH; 1.
DR    SMART; SM00208; TNFR; 3.
DR    PROSITE; PS00652; TNFR_NGFR_1; 3.
DR    PROSITE; PS50050; TNFR_NGFR_2; 2.
DR    PROSITE; PS50017; DEATH_DOMAIN; 1.
KW    Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
FT    SIGNAL        1     21       POTENTIAL.
FT    CHAIN        22    471       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT    DOMAIN       22    210       EXTRACELLULAR (POTENTIAL).
FT    TRANSMEM    211    233       POTENTIAL.
FT    DOMAIN      234    471       CYTOPLASMIC (POTENTIAL).
FT    DOMAIN       43    195       4 X TNFR-CYS.
FT    REPEAT       43     82       TNFR-CYS 1.
FT    REPEAT       83    125       TNFR-CYS 2.
FT    REPEAT      126    166       TNFR-CYS 3.
FT    REPEAT      167    195       TNFR-CYS 4.
FT    DOMAIN      340    360       N SMASE ACTIVATION DOMAIN (NSD).
FT    DOMAIN      372    457       DEATH.
FT    DISULFID     44     58       BY SIMILARITY.
FT    DISULFID     59     72       BY SIMILARITY.
FT    DISULFID     62     81       BY SIMILARITY.
FT    DISULFID     84     99       BY SIMILARITY.
FT    DISULFID    102    117       BY SIMILARITY.
FT    DISULFID    105    125       BY SIMILARITY.
FT    DISULFID    127    143       BY SIMILARITY.
FT    DISULFID    146    158       BY SIMILARITY.
FT    DISULFID    149    166       BY SIMILARITY.
FT    DISULFID    168    179       BY SIMILARITY.
FT    DISULFID    182    190       BY SIMILARITY.
FT    DISULFID    185    194       BY SIMILARITY.
FT    CARBOHYD     54     54       N-LINKED (GLCNAC       ) (POTENTIAL).
FT    CARBOHYD    145    145       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT    CARBOHYD    151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ    SEQUENCE   471 AA;  51367 MW;  5243EF514DFE81C4 CRC64;

  Query Match             71.7%;  Score 674.5;  DB 1;  Length 471;
  Best Local Similarity   71.6%;  Pred. No. 5e-49;
  Matches  111;  Conservative   17;  Mismatches   26;  Indels    1;  Gaps    1;

Qy          1 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 60
              :| |||||| ||||::|||||||||||||||||||||||:||||| |   |::|| ||||| ||
Db         41 ESPCPQGKYNHPQNSTCCTKCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCL 100

Qy         61 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 120
              ||||:|| ||' ||||| | ||||||||||||||| |        :: ||||' ||||:: |||
Db        101 SCSRCRDEMEQVEISPCIVVDRDTVCGCRKNQYRLYWSETHFQCLNCSLCPNGTVNIPCQE 160

Qy        121 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLC 155
              :|:|:| || ||||:   :|:|| :|    || ||
Db        161 RQDTICHCHMGFFLKGAKCISCHDCKNK-ECEKLC 194


RESULT   5
TNR1_RAT
ID   TNR1_RAT       STANDARD;      PRT;   461 AA.
AC   P22934;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-RI)
DE   (P55).
GN   TNFRSF1A OR TNFR1 OR TNFR-1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91050841; PubMed=1702294;
RA   Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA   Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT   "Molecular cloning and expression of human and rat tumor necrosis
RT   factor receptor chain (p60) and its soluble derivative, tumor
RT   necrosis factor-binding protein.";
RL   DNA Cell Biol. 9:705-715(1990).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M63122; AAA42256.1; -.
DR   PIR; B36555; B36555.
DR   HSSP; P19438; 1TNR.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 4.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    461       TUMOR NECROSIS FACTOR RECEPTOR 1.
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FT   DOMAIN        22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     212    234       POTENTIAL.
FT   DOMAIN       235    461       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        43    196       4 X TNFR-CYS.
FT   REPEAT        43     82       TNFR-CYS 1.
FT   REPEAT        83    125       TNFR-CYS 2.
FT   REPEAT       126    166       TNFR-CYS 3.
FT   REPEAT       167    196       TNFR-CYS 4.
FT   DOMAIN       344    354       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN       363    448       DEATH.
FT   DISULFID      44     58       BY SIMILARITY.
FT   DISULFID      59     72       BY SIMILARITY.
FT   DISULFID      62     81       BY SIMILARITY.
FT   DISULFID      84     99       BY SIMILARITY
FT   DISULFID     102    117       BY SIMILARITY.
FT   DISULFID     105    125       BY SIMILARITY.
FT   DISULFID     127    143       BY SIMILARITY.
FT   DISULFID     146    158       BY SIMILARITY.
FT   DISULFID     149    166       BY SIMILARITY.
FT   DISULFID     168    179       BY SIMILARITY.
FT   DISULFID     182    191       BY SIMILARITY.
FT   DISULFID     185    195       BY SIMILARITY.
FT   CARBOHYD      54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     201    201       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   461 AA;  50969 MW;  EB23C05450FBD202 CRC64;


  Query Match             71.1%;  Score 669;  DB 1;  Length 461;
  Best Local Similarity   68.3%;  Pred. No. 1.4e-48;
  Matches  110;  Conservative   19;  Mismatches   43;  Indels    0;  Gaps    0;

Qy       1 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL 60
           |::|||||| ||:|||||||||||||||| :||| |||:| |  |: |:||||:||:| ||
Db      41 DNLCPQGKYAHPKNNSICCTKCHKGIYLVSDCPSPGQFIVGFDCGTFTASQNHVRQCI 100

Qy      61 SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 120
           ||  ||||| ||||| |  | ||||||:|||:: | ||  ||| :|| | |||| : |:|
Db     101 SCKICRKEMPQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160

Qy     121 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIEN 161
           |||||| ||||||| ||| ||:|||: || ||||| : |
Db     161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVAN 201


RESULT   6
WSL1_HUMAN
ID   WSL1_HUMAN     STANDARD;      PRT;   417 AA.
AC   Q93038; Q93036; Q93037; Q92984; P78515; Q99831; Q99722; P78507;
AC   Q99830;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   WSL-1 PROTEIN PRECURSOR (APOPTOSIS MEDIATING RECEPTOR DR3) (APOPTOSIS-
DE   MEDIATING RECEPTOR TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PROTEIN)
DE   (APOPTOSIS INDUCING RECEPTOR AIR) (APO-3) (LYMPHOCYTE ASSOCIATED
DE   RECEPTOR OF DEATH) (LARD).
GN   TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DDR3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS.
RC   TISSUE=Lymphoid;
RX   MEDLINE=97088617; PubMed=8934525;
RA   Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,
RA   Grinham C.J., Brown R., Farrow S.N.;
RT   "A death domain-containing receptor that mediates apoptosis.";
RL   Nature 384:372-375(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Umbilical vein endothelial cells;
RX   MEDLINE=97081063; PubMed=8875942;
RA   Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,
RA   Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;
RT   "Signal transduction by DR3, a death domain-containing receptor
RT   related to TNFR-1 and CD95.";
RL   Science 274:990-992(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=97148200; PubMed=8994832;
RA   Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,
RA   Goddard A.D., Bauer K.D., Ashkenazi A.;
RT   "Apo-3, a new member of the tumor necrosis factor receptor family,
RT   contains a death domain and activates apoptosis and NF-kappa-B.";
RL   Curr. Biol. 6:1669-1676(1996).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97272273; PubMed=9114039;
RA   Screaton G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,
RA   McMichael A.J., Bell J.I.;
RT   "LARD: a new lymphoid-specific death domain containing receptor
RT   regulated by alternative pre-mRNA splicing.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
RN   [6]
RP   SEQUENCE OF 4-417 FROM N.A.
RC   TISSUE=Brain, and Fetal lung;
RX   MEDLINE=97205335; PubMed=9052839;
RA   Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
RA   Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,
RA   Browning J.L., Macdonald H.R., Tschopp J.;
RT   "TRAMP, a novel apoptosis mediating receptor with sequence homology
RT   to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
RL   Immunity 6:79-88(1997).
RN   [7]
RP   SEQUENCE OF 7-417 FROM N.A.
RC   TISSUE=Brain;
RA   Chaudhary P.M., Hood L.E.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: INDUCES APOPTOSIS AND ACTIVATES NUCLEAR FACTOR KAPPA-B
CC       (NF-KAPPAB). DIRECTLY INTERACTS WITH TRADD ADAPTATOR MOLECULE. MAY
CC       PLAY A ROLE IN REGULATING LYMPHOCYTE HOMEOSTASIS.
CC   -!- SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH
CC       THE TNFR1-ASSOCIATED MOLECULE TRADD AND THE TNFR1 RECEPTOR TO
CC       ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC   -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; WSL-1/LARD-1A (SHOWN HERE),
CC       WSL-S1/LARD-3 AND WSL-S2; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND
CC       LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS,
CC       COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
CC   -!- PTM: GLYCOSYLATED (PROBABLE).
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y09392; CAA70561.1; -.
DR   EMBL; Y09392; CAA70559.1; -.
DR   EMBL; Y09392; CAA70560.1; -.
DR   EMBL; U72763; AAC50819.1; -.
DR   EMBL; U83599; AAB41434.1; -.
DR   EMBL; U83600; AAB41435.1; -.
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DR   EMBL; U78029; AAB40918.1; -.
DR   EMBL; U74611; AAB39714.1; -.
DR   EMBL; U94501; AAC51306.1; -.
DR   EMBL; U94504; AAC51309.1; -.
DR   EMBL; U75380; AAC51192.1; -.
DR   EMBL; U75381; AAC51193.1; -.
DR   EMBL; U83597; AAB41432.1; -.
DR   HSSP; P19438; 1TNR.
DR   MIM; 603366; -.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Alternative splicing; Transmembrane; Signal;
KW   Repeat.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    417       WSL-1 PROTEIN.
FT   DOMAIN       25    199       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    200    220       POTENTIAL.
FT   DOMAIN      223    417       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       34    192       4 X TNFR-CYS.
FT   REPEAT       34     71       TNFR-CYS 1.
FT   REPEAT       72    115       TNFR-CYS 2.
FT   REPEAT      116    163       TNFR-CYS 3.
FT   REPEAT      164    192       TNFR-CYS 4.
FT   DOMAIN      332    413       DEATH.
FT   CARBOHYD     67     67       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    106    106       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    182    218       STLGSCPEFCAAVCGWRQMFWVQVLLAGLVVPLLLGA ->
FT                                VLGPCAPGWPCGPPPAWGHPDLHIPPLLASQAPCYCR (IN
FT                                ISOFORM WSL-S1).
FT   VARSPLIC    219    417       MISSING (IN ISOFORM WSL-S1).
FT   VARSPLIC    200    253       MFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG
FT                                MEALTPPPATHLS -> SRWCAGNARGFTGMDPGEAGEEGG
FT                                NHPTPTSCFQCSGSRCSWLALWSPSCLGPP (IN
FT                                ISOFORM WSL-S2).
FT   VARSPLIC    254    417       MISSING (IN ISOFORM WSL-S2).
FT   MUTAGEN     354    354       L->A: SUPPRESSES HOMODIMERIZATION, TNFR1
FT                                INTERACTION, AND APOPTOSIS INDUCTION.
FT   MUTAGEN     356    356       L->A: SUPPRESSES HOMODIMERIZATION, AND
FT                                TNFR1 INTERACTION.
FT   MUTAGEN     373    373       D->A: SUPPRESSES HOMODIMERIZATION, AND
FT                                TNFR1 INTERACTION.
FT   CONFLICT      4      6       RPR -> AAA (IN REF. 6).
FT   CONFLICT     60     60       P -> H (IN REF. 7).
FT   CONFLICT    167    167       P -> L (IN REF. 6 AND 7).
FT   CONFLICT    312    312       A -> R (IN REF. 1).
FT   CONFLICT    370    370       R -> L (IN REF. 1).
FT   CONFLICT    381    381       R -> H (IN REF. 1).
SQ   SEQUENCE   417 AA;  45385 MW;  5226319DFDB46706 CRC64;

  Query Match             21.3%;  Score 200.5;  DB 1;  Length 417;
  Best Local Similarity   29.8%;  Pred. No. 5.8e-10;
  Matches   48;  Conservative   20;  Mismatches   72;  Indels   21;  Gaps    7;

Qy        11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 69
             | :     ||  |  | ||   |  |  :: |  |   :| | |||     |  |  | ::
Db        40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99

Qy        70 GQVEISSCIVDRDIVCGCRKNQYRHYWSENLFQC-----FNCSLCLN-GIVH----LSCQ 119
              ||  :  :|:   || |||:     :         : ||      | |  ||: | .|     | |
Db       100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHIRLLCS 156

Qy       120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 155
              :     ||  ||:    : ||||       :| :    |  :|
Db       157 RRDIDCGICLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195

RESULT  7
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TNRC_HUMAN
ID   TNRC_HUMAN     STANDARD;      PRT;   435 AA.
AC   P36941;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   LYMPHOTOXIN BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
DE   2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR)
GN   LTBR OR TNFCR OR TNFRSF3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=93252381; PubMed=8486360;
RA   Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT   "Construction and evaluation of a hncDNA library of human 12p
RT   transcribed sequences derived from a somatic cell hybrid.";
RL   Genomics 16:214-218(1993).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=94225209; PubMed=8171323;
RA   Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA   Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT   "A lymphotoxin-beta-specific receptor.";
RL   Science 264:707-710(1994).
CC   -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN BETA. POSSIBLE FUNCTION IN
CC       IMMUNE DEVELOPMENT.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE RICH REGION.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; L04270; AAA36757.1; -.
DR   HSSP; P25942; 1CDF.
DR   MIM; 600979; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     30       POTENTIAL.
FT   CHAIN        31    435       LYMPHOTOXIN-BETA RECEPTOR.
FT   DOMAIN       31    227       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    228    248       POTENTIAL.
FT   DOMAIN      249    435       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       42    211       4 X TNFR-CYS.
FT   REPEAT       42     81       TNFR-CYS 1.
FT   REPEAT       82    124       TNFR-CYS 2.
FT   REPEAT      125    168       TNFR-CYS 3.
FT   REPEAT      169    211       TNFR-CYS 4.
FT   DISULFID     43     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     80       BY SIMILARITY.
FT   DISULFID     83     98       BY SIMILARITY.
FT   DISULFID    101    116       BY SIMILARITY.
FT   DISULFID    104    124       BY SIMILARITY.
FT   DISULFID    126    132       BY SIMILARITY.
FT   DISULFID    139    148       BY SIMILARITY.
FT   DISULFID    142    167       BY SIMILARITY.
FT   DISULFID    170    185       BY SIMILARITY.
FT   CARBOHYD     40     40       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    177    177       N-LINKED (GLCNAC. . .) (POTENTIAL).
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SQ   SEQUENCE   435 AA;  46709 MW;  624626E6022F656F CRC64;

  Query Match             19.9%;  Score 187.5;  DB 1;  Length 435;
  Best Local Similarity   32.7%;  Pred. No. 7.1e-09;
  Matches   49;  Conservative   17;  Mismatches   71;  Indels   13;  Gaps    7;

Qy          8 KYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRK 67
                :|  ||:  |||::|  |||:    |      :||  |   |    |:     |:|  |  |  |
Db         49 EYYEPQHR-ICCSRCPPGTYVSAKC-SRIRDIVCATCAENSYNEHWNYLTICQLCRPCDP 106

Qy         68 EMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSL---CLNGTVHLSCQE--KQ 122
                 ||  ||: ||   |  |  |  |:    :    |:     :|  :|  |    |   ||         |  |
Db        107 VMGLEEIAPCTSKRKTQCRCQPGMFCAAWA---LECTHCELLSDCPPGTEAELKDEVGKC 163

Qy        123 NTVCT-CHAGFFLRENECVSCSNCKKSLEC 151
                |  |  | || |  :|     : |:   |
Db        164 NNHCVPCKAGHF--QNTSSPSARCQPHIRC 191


RESULT    8
NGFR_HUMAN
ID   NGFR_HUMAN     STANDARD;      PRT;   427 AA.
AC   P08138;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE   (GP80-LNGFR) (P75 ICD).
GN   NGFR OR TNFRSF16.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87051725; PubMed=3022937;
RA   Johnson D., Lanahan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,
RA   Bothwell M., Chao M.;
RT   "Expression and structure of the human NGF receptor.";
RL   Cell 47:545-554(1986).
RN   [2]
RP   SEQUENCE OF 1-22 FROM N.A.
RX   MEDLINE=89096903; PubMed=2850481;
RA   Sehgal A., Patil N., Chao M.;
RT   "A constitutive promoter directs expression of the nerve growth factor
RT   receptor gene.";
RL   Mol. Cell. Biol. 8:3160-3167(1988).
CC   -!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
CC       NT-3, AND NT-4.
CC   -!- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
CC       BOND FORMATION.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; M14764; AAB59544.1; -.
DR   EMBL; M21621; AAA36363.1; -.
DR   PIR; A25218; GQHUN.
DR   HSSP; P07174; 1NGR.
DR   MIM; 162010; -.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
KW   Phosphorylation; Signal.
FT   SIGNAL        1     28
FT   CHAIN        29    427       LOW-AFFINITY NERVE GROWTH FACTOR
FT                                RECEPTOR.
FT   DOMAIN       29    250       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    251    272       POTENTIAL.
FT   DOMAIN      273    427       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       31    189       4 X TNFR-CYS.
FT   REPEAT       31     65       TNFR-CYS 1.
FT   REPEAT       66    107       TNFR-CYS 2.
FT   REPEAT      108    147       TNFR-CYS 3.
FT   REPEAT      148    189       TNFR-CYS 4.
FT   DOMAIN      344    421       DEATH.
FT   DISULFID     32     43       BY SIMILARITY.
FT   DISULFID     44     57       BY SIMILARITY.
FT   DISULFID     47     64       BY SIMILARITY.
FT   DISULFID     67     83       BY SIMILARITY.
FT   DISULFID     86     99       BY SIMILARITY.
FT   DISULFID     89    107       BY SIMILARITY.
FT   DISULFID    109    122       BY SIMILARITY.
FT   DISULFID    125    138       BY SIMILARITY.
FT   DISULFID    128    146       BY SIMILARITY.
FT   DISULFID    149    164       BY SIMILARITY.
FT   DISULFID    167    180       BY SIMILARITY.
FT   DISULFID    170    188       BY SIMILARITY.
FT   DOMAIN      197    248       SER/THR-RICH.
FT   CARBOHYD     60     60       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   427 AA;  45183 MW;  B09FA143FB3D625B CRC64;

  Query Match             19.4%;  Score 182.5;  DB 1;  Length 427;
  Best Local Similarity   32.1%;  Pred. No. 1.8e-08;
  Matches   52;  Conservative   25;  Mismatches   62;  Indels   23;  Gaps   11;

Qy          4 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCREC-ESGSFTASENHLRHCLSC 62
                || |  |  |      :   ||   |:  |   :      |  |    |  |  |    | :|  :|:      :       |  |
Db         32 CPTGLYTH--SGECCKACNLGEGVAQPC-GANQTVCEPCLDSVTFSDVVSATEPCKPC 86

Qy         63 SKCRKEMGQVEISS-CTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGT-VHLSCQE 120
                ::|     :|    :|: |     | || |     | .|   |    :|   |  :|   |: :   |||:
Db         87 TEC---VGLQSMSAPCVEADDAVCRC---AYGYYQDETTGRCEACRVCEAGSGLVFSCQD 140

Qy        121 KQNTVC-TCHAGFFLRE----NECVSCSNC----KKSLECIK 153
                ||||||  |  |  .  |     . |. |. |       ::  |||:
Db        141 KQNTVCEECPDGTYSDEANHVDPCLPCTVCEDTERQLRECTR 182


RESULT    9
TNR2_MOUSE
ID   TNR2_MOUSE     STANDARD;      PRT;   474 AA.
AC   P25119; P97893;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
GN   TNFRSF1B OR TNFR2 OR TNFR-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91187885; PubMed=1849278;
RA   Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA   Wong G.H., Chen E.Y., Goeddel D.V.;
RT   "Cloning and expression of cDNAs for two distinct murine tumor
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RT   necrosis factor receptors demonstrate one receptor is species
RT   specific.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91246168; PubMed 1645445;
RA   Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA   Copeland N.G., Jenkins N.A., Smith C.A.;
RT   "Molecular cloning and expression of the type 1 and type 2 murine
RT   receptors for tumor necrosis factor.";
RL   Mol. Cell. Biol. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE OF 1-26 FROM N.A.
RC   STRAIN=NOD;
RA   Jacob C.O., Liu J.;
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1-22 FROM N.A.
RC   TISSUE=Liver;
RA   Kissonerghis M., Fellowes R., Feldmann M., Chernajovsky Y.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; M60469; AAA39752.1; -.
DR   EMBL; M59378; AAA40463.1; -.
DR   EMBL; U39488; AAA85021.1; -.
DR   EMBL; X87128; CAA60618.1; -.
DR   PIR; B38634; B38634.
DR   HSSP; P19438; 1NCF.
DR   MGD; MGI:1314883; Tnfrsf1b.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     22
FT   CHAIN       23    474       TUMOR NECROSIS FACTOR RECEPTOR 2.
FT   DOMAIN      23    258       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    259   288       POTENTIAL.
FT   DOMAIN      289   474       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       39    203      4 X TNFR-CYS.
FT   REPEAT       39     77      TNFR-CYS 1.
FT   REPEAT       78    119      TNFR-CYS 2.
FT   REPEAT      120    164      TNFR-CYS 3.
FT   REPEAT      165    203      TNFR-CYS 4.
FT   DISULFID     40     54      BY SIMILARITY.
FT   DISULFID     55     68      BY SIMILARITY.
FT   DISULFID     58     76      BY SIMILARITY.
FT   DISULFID     79     94      BY SIMILARITY.
FT   DISULFID     97    111      BY SIMILARITY.
FT   DISULFID    101    119      BY SIMILARITY.
FT   DISULFID    121    127      BY SIMILARITY.
FT   DISULFID    136    145      BY SIMILARITY.
FT   DISULFID    139    163      BY SIMILARITY.
FT   DISULFID    166    181      BY SIMILARITY.
FT   CARBOHYD     69     69      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    195    195      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   474 AA;  50319 MW;  462EAE398C45E5E3 CRC64;
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  Query Match          19.2%;  Score 181;  DB 1;  Length 474;
  Best Local Similarity   31.7%;  Pred. No. 2.6e-05;
  Matches   51;  Conservative   20;  Mismatches   76;  Indels   14;  Gaps    8;

Qy       4 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC  62
           |  :  :  :   :|| ||  | |: : |     || | :|:  :|   :  | ||||
Db      40 CQISQEYYDRKAQMCCAKCPPGQYVKHFC-NKTSDTVCADCEASMYTQVWNQFRTCLSCS  98

Qy      63 SKCRKEMGQVEISSCTVDRDTVCGCKKNQY  92
           | |  : |||| :||  :: || |   :|     |  | :  ||   | |  |  |  |
Db      99 SSCTTD--QVETRACTKQQNRVCACEAGRYCALKTH--SGSCRQCMRLSKCGPGFGVASS 154

Qy     118 CQPKQNTVC 126
           |  :|  | | |   :  |  ||:   |: | :|
Db     155 RAPNGNVLCKACAPGTF- SDTTSSTDVCRPHRICSILAIP 193
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RESULT  10
VT2_MYXVI
ID   VT2_MYXVI      STANDARD;      PRT;   326 AA.
AC   P29825;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN   T2.
OS   Myxoma virus (strain Lausanne).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Leporipoxvirus.
OX   NCBI_TaxID=31530;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91335768; PubMed=1651597;
RA   Upton C., Macen J.L., Schreiber M., McFadden G.;
RT   "Myxoma virus expresses a secreted protein with homology to the tumor
RT   necrosis factor receptor gene family that contributes to viral
RT   virulence.";
RL   Virology 184:370-382(1991).
CC   -!- FUNCTION: BINDS TO TNF ALPHA AND BETA, PROBABLY PREVENTS TNF TO
CC       REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC       ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC   -!- SIMILARITY: CONTAINS A LA NGFR/TNFR TYPE CYSTEINE RICH REGION.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M95181; AAA46642.1; -.
DR   EMBL; A23729; CAA01688.1; -.
DR   PIR; A40566; G6VZML.
DR   HSSP; P19438; 1TNR.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     16       POTENTIAL.
FT   CHAIN       17    326       TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
FT   DOMAIN      27    186       4 X TNFR-CYS.
FT   REPEAT      27     62       TNFR-CYS 1.
FT   REPEAT      63    104       TNFR-CYS 2.
FT   REPEAT     105    147       TNFR-CYS 3.
FT   REPEAT     148    186       TNFR-CYS 4.
FT   CARBOHYD    66     66       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   181    181       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   205    205       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   238    238       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   326 AA;  35208 MW;  AB8E0276947292EF CRC64;
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  Query Match             19.1%;  Score 179.5;  DB 1;  Length 326;
  Best Local Similarity   27.4%;  Pred. No. 2.6e-08;
  Matches   51;  Conservative   19;  Mismatches   67;  Indels   49;  Gaps    7;

Qy      13 QNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC-SKCRKEMGQ 71
           : : :|||  |  |:|    | ||| || |  |:: :|||| ||   |:||  :|   :
Db      34 EKDGLCCISCPPGSYASRLC-GPGSDTVCSPCKNETFTASTNHAPACVSCRGRCTGHLS- 91

Qy      72 VEISSCTVDRDTVCGCRKNQY---------------------------------------- 92
             |  ||   || || |    |
Db      92 -ESQSCDKTRDRVCDCSAGNYC-LLKGQEGCRICAPKKKCPAGYGVSGHTRTGDVDCTKCP 150

Qy      93 RHYWSENLFQCFNCSLCLNG-IVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLEC 151
           |: :|: :    |:  |  :|  :    :| ||  ||     || |  |    :|
Db     151 RYIYSDAVSSTEICISSFNYISVEPNLYPVNDTSCTTTAG----PNEVVKTSEFSVTLNH 206

Qy     152 TKLCLP 157
           |  | |
Db     207 PD-CDP 211


RESULT  11
VT2_SFVKA
ID   VT2_SFVKA       STANDARD;       PRT;   325 AA.
AC   P25943;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN   T2.
OS   Shope fibroma virus (strain Kasza) (SFV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Leporipoxvirus.
OX   NCBI_TaxID=10272;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87321103; PubMed=2820128;
RA   Upton C., Delange A.M., McFadden G.;
RT   "Tumorigenic poxviruses: genomic organization and DNA sequence of the
RT   telomeric region of the Shope fibroma virus genome.";
RL   Virology 160:20-30(1987).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=91207415; PubMed=1850261;
RA   Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
RA   McFadden G., Goodwin R.G.;
RT   "T2 open reading frame from the Shope fibroma virus encodes a soluble
RT   form of the TNF receptor.";
RL   Biochem. Biophys. Res. Commun. 176:335-342(1991).
CC   -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC       REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC       ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR TYPE CYSTEINE-RICH REGION.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M17433; -; NOT_ANNOTATED_CDS.
DR   EMBL; A23727; CAA01687.1; -.
DR   PIR; B43692; B43692.
DR   HSSP; P19438; 1TNR.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     16       POTENTIAL.
FT   CHAIN       17    325       TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
FT   DOMAIN      27    186       4 X TNFR-CYS.
FT   REPEAT      27     62       TNFR-CYS 1.
FT   REPEAT      63    104       TNFR-CYS 2.
FT   REPEAT     105    147       TNFR-CYS 3.
FT   REPEAT     148    186       TNFR-CYS 4.
FT   CARBOHYD    105    105       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    181    181       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    205    205       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    238    238       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   325 AA;  35132 MW;  8105303399198A71E CRC64;


  Query Match             18.9%;  Score 178;  DB 1;  Length 325;
  Best Local Similarity   29.6%;  Pred. No. 3.4e-08;
  Matches   45,  Conservative   15,  Mismatches   62,  Indels   30;  Gaps    6;

Qy      13 QNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC-SKCRKEMGQ 71
           : : :||  || | |    | ||| :| |  || |:|||| ||   |:||   |   :
Db      34 EKDGLCCASCHPGFYASRLC-GPGSNTVCSPCEDGTFTASTNHAPACVSCRGPCTGHLS- 91

Qy      72 VEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGIVHLSCQEKQNTVCTCHAG 131
             |   |    | ||  |    |      :|      | :|   |                | ||
Db      92 -ESQPCDRTHDRVCNCSIGNYCLLKGQN-----GCRICAPQT-------------KCPAG 132

Qy     132 FFLRENECVSCSNCKK - ----SLECTKLC 155
           : :  :     : |:|        ||  |: |
Db     133 YGVSGHTRAGDTLCEKCPPHTYSDSLSPTERC 164


RESULT  12
FASA_PIG
ID   FASA_PIG        STANDARD;       PRT;   332 AA.
AC   O77736;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   FAS2 RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE   (APO-1 ANTIGEN) (CD95).
GN   TNFRSF6 OR APT1 OR FAS.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bartling B., Hoffmann J., Holtz J., Schulz R., Hensch G., Darmer D.;
RT   "Expression of apoptosis-associated genes in hibernating and stunned
RT   myocardium of pig.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC       ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC       RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC       SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC       ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC       CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC       APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC       INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC       SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC       AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
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CC   -----------------------------------------------------------------------
DR   EMBL; AJ001202; CAA04596.1; -.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17    332       FASL RECEPTOR.
FT   DOMAIN       17    175       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    176    192       POTENTIAL.
FT   DOMAIN      193    332       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       45    164       3 X TNFR-CYS.
FT   REPEAT       45     81       TNFR-CYS 1.
FT   REPEAT       82    125       TNFR-CYS 2.
FT   REPEAT      126    164       TNFR-CYS 3.
FT   DOMAIN      227    311       DEATH.
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    116    116       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   332 AA;  37592 MW;  5B8B03682755BE1B CRC64;

  Query Match             18.8%;  Score 176.5;  DB 1;  Length 332;
  Best Local Similarity   29.1%;  Pred. No. 4.7e-08;
  Matches   37;  Conservative   18;  Mismatches   65;  Indels    7;  Gaps    4;

Qy          1 DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESG-SFTASENHLRHC 59
                :| ||:|::     :       ||   |    |     : ||  ||     |   |   |  :|    :|    |
Db         43 FSFCPEGQH---RFGQFCCQPCPPCKRKHADCTSPGGAPQCVPCSEGEDYTDKNHHSSKC 99

Qy         60 LSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQ 119
                 |   |   | |         :||    ::| | |: | : |    :        |   |: | :|  .   .|
Db        100 RRCRVCDGFHGLEVEKNCTRTQNIKCRCKPNFFCH--TSQCEHCNPCTTCEHGVIE-NCT 156

Qy        120 EKQNTVC 126
                  || |
Db        157 PTSNTKC 163


RESULT 13
NGFR_RAT
ID   NGFR_RAT       STANDARD;      PRT;   425 AA.
AC   P07174;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-APR-1988 (Rel. 07, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE   (GP80-LNGFR) (P75 ICD).
GN   NGFR.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87115859; PubMed=3027580;
RA   Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;
RT   "Gene transfer and molecular cloning of the rat nerve growth factor
RT   receptor.";
RL   Nature 325:593-597(1987).
RN   [2]
RP   SEQUENCE OF 1-22 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=93077038; PubMed=1446821;
RA   Metsis M., Timmusk T., Allikmets R., Saarma M., Persson H.;
RT   "Regulatory elements and transcriptional regulation by testosterone
RT   of the rat nerve growth factor receptor promoter.";
RL   Gene 121:247-254(1992).
RN   [3]
RP   STRUCTURE BY NMR OF 334-418.
RX   MEDLINE=97449145; PubMed=9351641;
RA   Liepinsh E., Ilag L.L., Otting G., Ibanez C.F.;
RT   "NMR structure of the death domain of the p75 neurotrophin receptor.";
RL   EMBO J. 16:4999-5005(1997).
CC   -!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
CC       NT-3, AND NT 4.
CC   -!- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
CC       BOND FORMATION.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC   -!- SIMILARITY: CONTAINS A LA NGFR/TNFR TYPE CYSTEINE RICH REGION.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   -----------------------------------------------------------------------
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CC   -----------------------------------------------------------------------
DR   EMBL; X05137; CAA28783.1; -.
DR   EMBL; X61263; -; NOT_ANNOTATED_CDS.
DR   PIR; A26431; A26431.
DR   PDB; 1NGR; 29-JUL-97.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
KW   Phosphorylation; Signal; 3D structure.
FT   SIGNAL        1     29
FT   CHAIN        30    425       LOW AFFINITY NERVE GROWTH FACTOR
FT                                RECEPTOR.
FT   DOMAIN       30    251       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    252    273       POTENTIAL.
FT   DOMAIN      274    425       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       32    190       4 X TNFR-CYS.
FT   REPEAT       32     66       TNFR-CYS 1.
FT   REPEAT       67    108       TNFR-CYS 2.
FT   REPEAT      109    148       TNFR-CYS 3.
FT   REPEAT      149    190       TNFR-CYS 4.
FT   DOMAIN      198    249       SER/THR-RICH.
FT   DOMAIN      354    419       DEATH.
FT   DISULFID     33     44       BY SIMILARITY.
FT   DISULFID     45     58       BY SIMILARITY.
FT   DISULFID     48     65       BY SIMILARITY.
FT   DISULFID     68     84       BY SIMILARITY.
FT   DISULFID     87    100       BY SIMILARITY.
FT   DISULFID     90    108       BY SIMILARITY.
FT   DISULFID    110    123       BY SIMILARITY.
FT   DISULFID    126    139       BY SIMILARITY.
FT   DISULFID    129    147       BY SIMILARITY.
FT   DISULFID    150    165       BY SIMILARITY.
FT   DISULFID    168    181       BY SIMILARITY.
FT   DISULFID    171    189       BY SIMILARITY.
FT   CARBOHYD     61     61       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     71     71       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   425 AA;  45432 MW;  B2F152D94D3827F8 CRC64;

  Query Match             18.8%;  Score 176.5;  DB 1;  Length 425;
  Best Local Similarity   30.9%;  Pred. No. 5.7e-08;
  Matches   59;  Conservative   25;  Mismatches   88;  Indels   19;  Gaps   10;
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Qy       4 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSC 63
           |  | | |   :  ||  |: |  :   | |  | | |  | :: :|:   :    | |
Db      33 CSIGLYIH---SGECCKACNLGEGVAQPC-GANQ-TVCEPCLDSVTFSDVVSAEPCKPC 87

Qy      64 KCPKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGT-VHLSCQEK 122
           ::|   :|   :|: |    | || |    | :|  |    |  ||:|  |: :  |||:
Db      88 TEC---LGLQSMSAPCVEADDAVCRC---AYGYYQDEETGHCEACSVCEVGSGLVFSCQD 141

Qy     123 KQNTVC-TCHAGFFLREN----NECVSCSNCKKSLECTKLCLP 157
           |||||  |  | :  |     : |: |: | :    : | |
Db     142 KQNTVCEECPEGTYSDEANHVDPCLPCTVCEDTERQLRECTR 183


RESULT  14
CD40_MOUSE
ID   CD40_MOUSE     STANDARD;      PRT;   289 AA.
AC   P27512;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-OCT-1996 (Rel. 34, Last Sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
GN   TNFRSF5 OR CD40.
OS   Mus musculus (Mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciuroqnathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92105763; PubMed=1370315;
RA   Torres R.M., Clark E.A.;
RT   "Differential increase of an alternatively polyadenylated mRNA
RT   species of murine CD40 upon B lymphocyte activation.";
RL   J. Immunol. 148:620-626(1992).
RN   [2]
RP   REVISIONS.
RC   STRAIN=BALB/C;
RA   Torres R.M.;
RL   Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=Liver;
RX   MEDLINE=93094586; PubMed=1281194;
RA   Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
RA   Howard M., Cockayne D.A.;
RT   "Genomic structure and chromosomal mapping of the murine CD40 gene.";
RL   J. Immunol. 149:3921-3926(1992).
CC   -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
CC   ----------------------------------------- -----------------------------
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CC   or send an email to license@isb-sib.ch)
CC   ----------------------------------------------------------------------
DR   EMBL; M83312; AAB08705.1; -.
DR   EMBL; M94126; AAA37404.1; -.
DR   EMBL; M94129; AAA37404.1; JOINED.
DR   EMBL; M94128; AAA37404.1; JOINED.
DR   EMBL; M94127; AAA37404.1; JOINED.
DR   PIR; A46476; A46476.
DR   HSSP; P25942; 1CDT.
DR   MGD; MGI:88336; Inirs15.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 4.
KW   Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT   SIGNAL       1     19       POTENTIAL.
FT   CHAIN       20    289       CD40L RECEPTOR.
FT   DOMAIN      20    193       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   194    215       POTENTIAL.
FT   DOMAIN     216    289       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      25    187       4 X TNFR-CYS.
FT   REPEAT      25     60       TNFR-CYS 1.
FT   REPEAT      61    103       TNFR-CYS 2.
FT   REPEAT     104    144       TNFR-CYS 3.
FT   REPEAT     145    187       TNFR-CYS 4.
FT   CARBOHYD   153    153       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   289 AA;  32111 MW;  C791CB6D2FEA574E CRC64;


  Query Match             17.8%;  Score 167.5;  DB 1;  Length 289;
  Best Local Similarity   29.9%;  Pred. No. 2.3e-07;
  Matches   46;  Conservative   23;  Mismatches   72;  Indels   13;  Gaps    7;

Qy       4 CPQGKYIHPQNNSICCTKCHKGIYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 63
           |   :|:|    :  ||  |  |: | : |    : | |  |:|| |:|  |    |
Db      26 CSDKQYLH---DGQCCDLCQPGSRLVSHCTAL-EKTQCHPCDSGEFSAQWNREIRCHQHR 81

Qy      64 KCPKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGT-VHLSCQEKQ 122
           |   |     | : |||| }:: |  |  |::   |   : |: |  |     |
Db      82 HCEPNQGLRVKKEGIAESDTVCTCKEGQ--HCISKDCEACAQHTPCIPGFGVMEMATETT 139

Qy     123 NTVC-TCHAGFFLREN----ECVSCSNCK-KSLE 150
           :|||  |  |||  ::    :|   ::|: |:||
Db     140 DTVCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLE 173


RESULT  15
TNRC_MOUSE
ID   TNRC_MOUSE     STANDARD;      PRT;   415 AA.
AC   P50284;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
GN   LTBR OR TNFCR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciuroqnathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CVB; TISSUE=Lung;
RX   MEDLINE=96072804; PubMed=7594541;
RA   Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA   Browning J.L., Ware C.F.;
RT   "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT   and expression.";
RL   J. Immunol. 155:5280-5288(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96163885; PubMed=8586432;
RA   Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA   Honjo T.;
RT   "The murine lymphotoxin beta receptor cDNA: isolation by the signal
RT   sequence trap and chromosomal mapping.";
RL   Genomics 30:312-319(1995).
CC   -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC       IMMUNE DEVELOPMENT.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR TYPE CYSTEINE RICH REGION.
CC   ----------------------------------------- -----------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; U29173; AAA68964.1; -.
DR   EMBL; L38423; AAB00846.1; -.
DR   EMBL; U30798; AAA81344.1; -.
DR   HSSP; P25942; 1CDF.
DR   MGD; MGI:104875; Ltbr.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     30       POTENTIAL.
FT   CHAIN        31    415       LYMPHOTOXIN-BETA RECEPTOR.
FT   DOMAIN       31    223       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    224    244       POTENTIAL.
FT   DOMAIN      245    415       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       42    213       4 X TNFR-CYS.
FT   REPEAT       42     81       TNFR-CYS 1.
FT   REPEAT       82    124       TNFR-CYS 2.
FT   REPEAT      125    170       TNFR-CYS 3.
FT   REPEAT      171    213       TNFR-CYS 4.
FT   DISULFID     43     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     80       BY SIMILARITY.
FT   DISULFID     83     98       BY SIMILARITY.
FT   DISULFID    101    116       BY SIMILARITY.
FT   DISULFID    104    124       BY SIMILARITY.
FT   DISULFID    126    132       BY SIMILARITY.
FT   DISULFID    139    150       BY SIMILARITY.
FT   DISULFID    142    169       BY SIMILARITY.
FT   DISULFID    172    187       BY SIMILARITY.
FT   CARBOHYD     40     40       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    179    179       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   415 AA;  44956 MW;  29B326A566AEF661 CRC64;


  Query Match             17.8%;  Score 167.5;  DB 1;  Length 415;
  Best Local Similarity   27.6%;  Pred. No. 3.1e-07;
  Matches   42;  Conservative   21;  Mismatches   74;  Indels   15;  Gaps    6;

Qy       8 KYTHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRK 67
           :|  | :: :|||:|  | :::  |    ||| |: |   |:    |||  |  |  |
Db      49 EYYEPMHD-VCCSRCPPGEFVFAVC-SKSQDTVCKTCPHNSYNEHWNHLSTCQLCKPCDT 106

Qy      68 EMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCS-----LCLNGTVHLSCQEKQ 122
            :|  |:: || ||   | |:       |      :| :|      ||  ||      |
Db     107 VLGFEEVAPCTSDRKAECRCQPGMSCVYLDN---ECVHCEEERLVLCQPGTEAEVTDEIM 163

Qy     123 NT---VCICHAGFFLRENECVSCSNCKKSLEC 151
           :|      |  | |  :|     : |:    |
Db     164 DTDVNCVPCKPGHF--QNTSSPFARCQPHTRC 193


Search completed: April 24, 2002, 10:49:10
Job time: 672 sec
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